

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/563,896

Source: IFW

Date Processed by STIC: 8/25/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 08/25/2006

PATENT APPLICATION: US/10/563,896

TIME: 12:09:06

Input Set : E:\seq_490051_402uspc.app.txt

Output Set : N:\CRF4\08252006\J563896.raw

3 <110> APPLICANT: TAKEDA, Junji
 4 HORIE, Kyoji
 6 <120> TITLE OF INVENTION: METHOD OF PREPARING TRANSGENIC ORGANISM WITH USE OF METHYLATION

7 AND SYTEM THEREFOR
 9 <130> FILE REFERENCE: 490051.402USPC
 11 <140> CURRENT APPLICATION NUMBER: US 10/563,896
 C--> 12 <141> CURRENT FILING DATE: 2006-01-09
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/010090
 15 <151> PRIOR FILING DATE: 2004-07-08
 17 <160> NUMBER OF SEQ ID NOS: 76
 19 <170> SOFTWARE: PatentIn version 3.2
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1455
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Tanichthys albonubes
 27 <220> FEATURE:
 28 <221> NAME/KEY: misc_feature
 29 <222> LOCATION: (1)..(1455)
 30 <223> OTHER INFORMATION: /note="Tc1-like transposon"
 32 <300> PUBLICATION INFORMATION:
 33 <308> DATABASE ACCESSION NO: L48685
 34 <309> DATABASE ENTRY DATE: 1996-05-31
 35 <313> RELEVANT RESIDUES: (1)..(1455)
 37 <400> SEQUENCE: 1

see
p.6

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38 cagttgaagt cggaagttta catacactta agttggagtc attaaaactc gtttttcaac      60
40 tacaccacaa atttcttggt aacaaacaat agttttggca agtcagttag gacatctact      120
42 ttgtgcatga cacaagtcac ttttccaaca attgtttaca gacagattat ttcacttata      180
44 attcactgta tcacaattcc agtgggtcag aagtttacat acactaagtt gactgtgcct      240
46 ttaaacagct tggaaaattc cagaaaatga tgtcatggct ttagaagctt ctgatagact      300
48 aattgacatc atttgagtca attggagggtg tacctgtgga tgtatttcaa ggcctacctt      360
50 caaacgcagt gcctctttgc ttgacataat gggaaaatca aaagaaatca gccaacacca      420
52 tgggaccacg cagccgtcat accgctcagg aatgagacgc attctgtctc ctagagataa      480
54 acatactgtg gtgcgaaaag tgcaaatcaa tcccagaacg acagcaaagg accttgtaga      540
56 gatgctggag aaaacaggta tgaatgtttc tatatccaca gtaaaaacga gtcctatatc      600
58 gacataacct gaaaggccgc tcagcaagga agaagccact gtcccaaaac cgccataaaa      660
60 aagccagact acggtttgca actgcacatg gggacaaata tgggtacttt tggagaaatg      720
62 tcctctcttc tgggtctgatg aaaaaaaaat agaactatct ggcataatg accatcggtta      780
64 tgtttggagg aaaaaggggg agcttgcaag ccgaagatca ccatcccaag cgtgaagcac      840
66 ggggggtggc gcatcatggt gtgggggtgc tttgctgcag gagggactgg tgcacttcac      900
68 aaaatagatg gcatcatgac aaaggaaaat tatgtggcta tattgaagca acatctcaag      960
70 acatcagtca ggaagttcaa gcttggtcac aaatgggtct tccaaatgga caatgacctc     1020
72 aagcatactt ccaaagttgt ggcaaaatgg cttaaggtca acaaagtcaa ggtattggag     1080
74 tggccatcac aaagctctga cctcaatcct atagaaagga ggaatgagcc aaaattcacc     1140

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76 caacttattg tgggaagctt gtggaaggct actcgaaatg tttgacccaa gttaaacaat 1200
78 ttaaaggcaa tgctaccaa tactaattga gtgtatgta acttctgacc cactgggaat 1260
80 gtgatgaaag aaataaaagc tgaaatgaat cattctctct actattattc tgatatttca 1320
82 cattcttaaa ataaagtggg gatcctaact gaccttaaga cagggaatct ttactcggat 1380
84 taaatgtcag gaattgtgaa aaagtgaagt taaatgtatt tggctaagggt gtatgtaaac 1440
86 ttccgacttc aactg 1455
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 1023
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Sleeping Beauty transposase
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (1)..(1023)
102 <220> FEATURE:
103 <221> NAME/KEY: misc_feature
104 <222> LOCATION: (1)..(1023)
105 <223> OTHER INFORMATION: Sleeping Beauty transposase
107 <400> SEQUENCE: 2
108 atg gga aaa tca aaa gaa atc agc caa gac ctc aga aaa aaa att gta 48
109 Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
110 1 5 10 15
112 gac ctc cac aag tct ggt tca tcc ttg gga gca att tcc aaa cgc ctg 96
113 Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
114 20 25 30
116 aaa gta cca cgt tca tct gta caa aca ata gta cgc aag tat aaa cac 144
117 Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
118 35 40 45
120 cat ggg acc acg cag ccg tca tac cgc tca gga agg aga cgc gtt ctg 192
121 His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
122 50 55 60
124 tct cct aga gat gaa cgt act ttg gtg cga aaa gtg caa atc aat ccc 240
125 Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
126 65 70 75 80
128 aga aca aca gca aag gac ctt gtg aag atg ctg gag gaa aca ggt aca 288
129 Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
130 85 90 95
132 aaa gta tct ata tcc aca gta aaa cga gtc cta tat cga cat aac ctg 336
133 Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
134 100 105 110
136 aaa ggc cgc tca gca agg aag aag cca ctg ctc caa aac cga cat aag 384
137 Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
138 115 120 125
140 aaa gcc aga cta cgg ttt gca act gca cat ggg gac aaa gat cgt act 432
141 Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
142 130 135 140
144 ttt tgg aga aat gtc ctc tgg tct gat gaa aca aaa ata gaa ctg ttt 480
145 Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe

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146 145          150          155          160
148 ggc cat aat gac cat cgt tat gtt tgg agg aag aag ggg gag gct tgc      528
149 Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
150          165          170          175
152 aag ccg aag aac acc atc cca acc gtg aag cac ggg ggt ggc agc atc      576
153 Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
154          180          185          190
156 atg ttg tgg ggg tgc ttt gct gca gga ggg act ggt gca ctt cac aaa      624
157 Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
158          195          200          205
160 ata gat ggc atc atg agg aag gaa aat tat gtg gat ata ttg aag caa      672
161 Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
162          210          215          220
164 cat ctc aag aca tca gtc agg aag tta aag ctt ggt cgc aaa tgg gtc      720
165 His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
166 225          230          235          240
168 ttc caa atg gac aat gac ccc aag cat act tcc aaa gtt gtg gca aaa      768
169 Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
170          245          250          255
172 tgg ctt aag gac aac aaa gtc aag gta ttg gag tgg cca tca caa agc      816
173 Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
174          260          265          270
176 cct gac ctc aat cct ata gaa aat ttg tgg gca gaa ctg aaa aag cgt      864
177 Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
178          275          280          285
180 gtg cga gca agg agg cct aca aac ctg act cag tta cac cag ctc tgt      912
181 Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
182          290          295          300
184 cag gag gaa tgg gcc aaa att cac cca act tat tgt ggg aag ctt gtg      960
185 Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
186 305          310          315          320
188 gaa ggc tac ccg aaa cgt ttg acc caa gtt aaa caa ttt aaa ggc aat      1008
189 Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
190          325          330          335
192 gct acc aaa tac tag      1023
193 Ala Thr Lys Tyr
194          340
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 340
199 <212> TYPE: PRT
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Synthetic Construct
205 <400> SEQUENCE: 3
207 Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
208 1          5          10          15
211 Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
212          20          25          30
215 Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His

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216          35          40          45
219 His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
220          50          55          60
223 Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
224 65          70          75          80
227 Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
228          85          90          95
231 Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
232          100          105          110
235 Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
236          115          120          125
239 Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
240          130          135          140
243 Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
244 145          150          155          160
247 Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
248          165          170          175
251 Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
252          180          185          190
255 Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
256          195          200          205
259 Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
260          210          215          220
263 His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
264 225          230          235          240
267 Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
268          245          250          255
271 Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
272          260          265          270
275 Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
276          275          280          285
279 Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
280          290          295          300
283 Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
284 305          310          315          320
287 Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
288          325          330          335
291 Ala Thr Lys Tyr
292          340
295 <210> SEQ ID NO: 4
296 <211> LENGTH: 26
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Left outside sequence
303 <400> SEQUENCE: 4
304 gttgaagtcg gaagtttaca cttagg
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 30

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RAW SEQUENCE LISTING

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Input Set : E:\seq_490051_402uspc.app.txt

Output Set: N:\CRF4\08252006\J563896.raw

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309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Left inside sequence
315 <400> SEQUENCE: 5
316 ccagtgggtc agaagtttac atacactaag 30
319 <210> SEQ ID NO: 6
320 <211> LENGTH: 27
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence;
324 <220> FEATURE:
325 <223> OTHER INFORMATION: TgTP-1U
327 <400> SEQUENCE: 6
328 gaccgcttcc tcgtgcttta cggtatc 27
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 30
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence;
336 <220> FEATURE:
337 <223> OTHER INFORMATION: TgTP-2L
339 <400> SEQUENCE: 7
340 acacaggaaa cagctatgac catgattacg 30
343 <210> SEQ ID NO: 8
344 <211> LENGTH: 30
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence;
348 <220> FEATURE:
349 <223> OTHER INFORMATION: TgTP-2U
351 <400> SEQUENCE: 8
352 tctatcgctt tcttgacgag ttcttctgag 30
355 <210> SEQ ID NO: 9
356 <211> LENGTH: 28
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence;
360 <220> FEATURE:
361 <223> OTHER INFORMATION: TgTP-3L
363 <400> SEQUENCE: 9
364 caagcgcgca attaacccctc actaaagg 28
367 <210> SEQ ID NO: 10
368 <211> LENGTH: 1610
369 <212> TYPE: DNA
370 <213> ORGANISM: Caenorhabditis elegans
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (1)..(1610)
376 <223> OTHER INFORMATION: Transposon="Tc1"
378 <220> FEATURE:
379 <221> NAME/KEY: CDS
380 <222> LOCATION: (523)..(1344)

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/563,896

DATE: 08/25/2006
TIME: 12:09:07

Input Set : E:\seq_490051_402uspc.app.txt
Output Set: N:\CRF4\08252006\J563896.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:64; N Pos. 13

Seq#:65; N Pos. 21

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43

Seq#:44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67

Seq#:68,69,70,71,72,73,74,75,76

VERIFICATION SUMMARY

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Input Set : E:\seq_490051_402uspc.app.txt

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0

L:2105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0